

SCORE Search Results Details for Application 10762154 and Search Result us-10-762-154-1.rge.

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This page gives you Search Results detail for the Application 10762154 and Search Result us-10-762-154-1.rge.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 10, 2006, 11:50:08 ; Search time 9168 Seconds
(without alignments)
5764.893 Million cell updates/sec

Title: US-10-762-154-1
Perfect score: 2845
Sequence: 1 MRDYDEVIAFLGEWGPPQRL.....KKTRDSMETEENPKVLITAF 551

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03h
-USER=US10762154 @CGN_1_1_5683 @runat_09082006_171710_2444 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 2: gb_pat:*
- 3: gb_ph:*
- 4: gb_pl:*
- 5: gb_pr:*
- 6: gb_ro:*
- 7: gb_sts:*
- 8: gb_sy:*
- 9: gb_un:*
- 10: gb_vi:*
- 11: gb_ov:*
- 12: gb_htg:*
- 13: gb_in:*
- 14: gb_om:*
- 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2845	100.0	2135	2	CS059053	CS059053 Sequence
2	2845	100.0	2135	2	AR563472	AR563472 Sequence
3	2845	100.0	2135	5	AB007448	AB007448 Homo sapi
4	2833	99.6	2166	2	CS240059	CS240059 Sequence
5	2833	99.6	2166	5	HSPIMTP	Y09881 Homo sapien
6	2833	99.6	2214	2	AR533635	AR533635 Sequence
7	2833	99.6	2214	2	AX799152	AX799152 Sequence
8	2833	99.6	2214	5	BC028313	BC028313 Homo sapi
9	2820	99.1	2136	2	CQ721604	CQ721604 Sequence
10	2783	97.8	2136	2	AR533668	AR533668 Sequence
11	2783	97.8	2136	2	AX799188	AX799188 Sequence
12	2484	87.3	2258	6	AF169831	AF169831 Rattus no
13	2470	86.8	2083	2	AR563491	AR563491 Sequence
14	2470	86.8	2083	6	AB016257	AB016257 Mus muscu
15	2470	86.8	2277	6	BC010590	BC010590 Mus muscu
16	2218	78.0	1831	2	CS239323	CS239323 Sequence
17	2218	78.0	1831	2	AR563473	AR563473 Sequence
18	2218	78.0	1831	2	AR581446	AR581446 Sequence
19	2218	78.0	1831	5	AB015050	AB015050 Homo sapi
20	2218	78.0	3252	2	CS059038	CS059038 Sequence
21	2218	78.0	3252	2	CS239179	CS239179 Sequence
22	2218	78.0	3252	2	AR533636	AR533636 Sequence
23	2218	78.0	3252	2	AX799154	AX799154 Sequence
24	2218	78.0	3252	5	AF057164	AF057164 Homo sapi
25	2218	78.0	3254	2	CQ490432	CQ490432 Sequence
26	2218	78.0	3254	2	CQ496283	CQ496283 Sequence
27	2211	77.7	2811	5	BC012325	BC012325 Homo sapi
28	2176.5	76.5	3232	14	BC105377	BC105377 Bos tauru
29	2165	76.1	3007	6	RNAJ1933	AJ001933 Rattus no
30	2165	76.1	3037	6	AF110416	AF110416 Rattus no
31	2164	76.1	1881	6	AF111425	AF111425 Mus muscu
32	2164	76.1	1888	2	AR563495	AR563495 Sequence
33	2164	76.1	1888	2	AR581447	AR581447 Sequence
34	2164	76.1	1888	6	AB015800	AB015800 Mus muscu
35	2164	76.1	2621	6	AF110417	AF110417 Mus muscu
36	2164	76.1	3111	6	BC031118	BC031118 Mus muscu
37	2159	75.9	3240	2	CQ721601	CQ721601 Sequence
38	2152	75.6	3038	6	AB017260	AB017260 Rattus no
39	2034.5	71.5	2297	6	AB018436	AB018436 Mus muscu
40	2033	71.5	2243	11	BC056014	BC056014 Xenopus l
41	1914	67.3	3469	11	CR855437	CR855437 Xenopus t
42	1913	67.2	2378	11	BC063904	BC063904 Xenopus t
43	1772.5	62.3	5504	11	BC082839	BC082839 Xenopus l
44	1570.5	55.2	2926	6	DQ119106	DQ119106 Rattus no
45	1428.5	50.2	1750	11	BC062384	BC062384 Danio rer

ALIGNMENTS

RESULT 1
CS059053
LOCUS CS059053 2135 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 1 from Patent WO2005026737.
ACCESSION CS059053
VERSION CS059053.1 GI:62551899
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Golz,S., Brueggemeier,U. and Geerts,A.
TITLE Diagnostics and therapeutics for diseases associated with
organisation transporter slc22a4 (slc22a4)
JOURNAL Patent: WO 2005026737-A 1 24-MAR-2005;
Bayer HealthCare AG (DE)
FEATURES
source Location/Qualifiers
1..2135
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Alignment Scores:

Pred. No.: 1.27e-284 Length: 2135
Score: 2845.00 Matches: 551

SCORE Search Results Details for Application 10762154 and Search Result us-10-762-154-1.rng.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 10, 2006, 11:49:29 ; Search time 822 Seconds
(without alignments)
7010.418 Million cell updates/sec

Title: US-10-762-154-1
Perfect score: 2845
Sequence: 1 MRDYDEVIAFLGEWGPFQRL.....KKTRDSMETEENPKVLITAF 551

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p
-USER=US10762154 @CGN_1_1_1147 @runat_09082006_171709_2433 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_8:*
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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2845	100.0	1736	8	ABZ24259	Abz24259 Human SLC
2	2845	100.0	2135	2	AAX26879	Aax26879 DNA encod
3	2845	100.0	2135	8	ABZ24257	Abz24257 Human SLC
4	2845	100.0	2135	14	ADY84981	Ady84981 Human org
5	2833	99.6	2135	8	ABZ24258	Abz24258 Human SLC
6	2833	99.6	2166	8	ABZ24256	Abz24256 Human SLC
7	2833	99.6	2166	15	AEE33284	Aee33284 DNA encod
8	2833	99.6	2214	14	ADZ49182	Adz49182 Insulin s
9	2783	97.8	2136	9	ACF05052	Acf05052 Human cat
10	2470	86.8	2083	2	AAX26898	Aax26898 DNA encod
11	2470	86.8	2083	14	ADZ62649	Adz62649 Murine Sl
12	2218	78.0	1674	14	ADV43783	Adv43783 Human psy
13	2218	78.0	1831	2	AAX26880	Aax26880 DNA encod
14	2218	78.0	1831	3	AAA09889	Aaa09889 Human OCT
15	2218	78.0	1831	8	ABZ24261	Abz24261 Human SLC
16	2218	78.0	1831	8	ACD13415	Acd13415 Human DNA
17	2218	78.0	1831	15	AEE60942	Aee60942 Human pat
18	2218	78.0	3051	10	ADE07453	Ade07453 Novel cod
19	2218	78.0	3252	8	ABZ24262	Abz24262 Human SLC
20	2218	78.0	3252	13	ADP23816	Adp23816 PRO polyp
21	2218	78.0	3252	14	ADY79866	Ady79866 Nucleotid
22	2218	78.0	3252	14	ADZ49183	Adz49183 Insulin s
23	2218	78.0	3252	15	AEE60798	Aee60798 Human pat
24	2218	78.0	3254	5	ABV22306	Abv22306 Human pro
25	2218	78.0	3254	5	ABV28137	Abv28137 Human pro
c 26	2218	78.0	3261	5	AAS67216	Aas67216 DNA encod
c 27	2218	78.0	3261	10	ADE09665	Ade09665 Novel DNA
c 28	2218	78.0	3261	10	ADE09605	Ade09605 Novel DNA
29	2211	77.7	2811	8	ABZ24260	Abz24260 Human SLC
30	2165	76.1	3037	10	ADB58358	Adb58358 Toxicity-
31	2165	76.1	3037	10	ADB52930	Adb52930 Primary r
32	2164	76.1	1888	2	AAX26902	Aax26902 DNA encod
33	2164	76.1	1888	3	AAA09890	Aaa09890 Mouse OCT
34	2164	76.1	2621	14	ADZ62487	Adz62487 Murine Sl
35	2152	75.6	3038	12	ADP71869	Adp71869 Renal tox
36	2034.5	71.5	2297	3	AAA88053	Aaa88053 Mouse OCT
37	2034.5	71.5	2297	14	ADZ62288	Adz62288 Murine Sl
38	1570.5	55.2	2928	12	ADL17760	Adl17760 Organic c
39	857	30.1	2533	4	ABL10925	Abl10925 Drosophil
40	857	30.1	4533	4	ABL10924	Abl10924 Drosophil
41	819	28.8	2087	4	ABL23075	Abl23075 Drosophil
42	819	28.8	4087	4	ABL23074	Abl23074 Drosophil
43	797.5	28.0	1924	6	ABZ33731	Abz33731 Human TRI
44	797.5	28.0	2110	4	AAK51500	Aak51500 Human pol
45	794.5	27.9	1734	10	ADC77506	Adc77506 Human org

ALIGNMENTS

RESULT 1

ABZ24259

ID ABZ24259 standard; DNA; 1736 BP.

XX

AC ABZ24259;

XX

DT 14-APR-2003 (first entry)

XX

DE Human SLC22A gene related DNA (sequence Id no. 19).

XX

KW SLC22A; transporter; p53; cytostatic; cancer; human; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200299053-A2.

XX

PD 12-DEC-2002.

XX

PF 03-JUN-2002; 2002WO-US017456.

XX

PR 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0328605P.

PR 15-FEB-2002; 2002US-0357253P.

XX

PA (EXEL-) EXELIXIS INC.

XX

PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;

PI Lioubin MN;

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 10, 2006, 11:56:27 ; Search time 305 Seconds
(without alignments)
5070.398 Million cell updates/sec

Title: US-10-762-154-1
Perfect score: 2845
Sequence: 1 MRDYDEVIAFLGEWGPFQRL.....KKTRDSMETEENPKVLITAF 551

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-HOST=abss03h -USER=US10762154 @CGN_1_1_204 @runat_09082006_171714_2536
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database : Issued Patents NA:*

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4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
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9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
%					
Result	Query				
No.	Score	Match	Length	ID	Description
1	2845	100.0	2135	3 US-09-521-195B-2	Sequence 2, Appli

2	2833	99.6	2214	3	US-10-327-189-1	Sequence 1, Appli
3	2783	97.8	2136	3	US-10-327-189-37	Sequence 37, Appl
4	2470	86.8	2083	3	US-09-521-195B-23	Sequence 23, Appl
5	2218	78.0	1831	3	US-09-521-195B-4	Sequence 4, Appli
6	2218	78.0	1831	3	US-09-798-743-2	Sequence 2, Appli
7	2218	78.0	3252	3	US-10-327-189-3	Sequence 3, Appli
8	2218	78.0	3252	3	US-09-949-016-438	Sequence 438, App
9	2166	76.1	3223	3	US-09-949-016-2058	Sequence 2058, Ap
10	2164	76.1	1888	3	US-09-521-195B-28	Sequence 28, Appl
11	2164	76.1	1888	3	US-09-798-743-4	Sequence 4, Appli
12	704.5	24.8	1896	3	US-08-501-572-6	Sequence 6, Appli
13	704.5	24.8	1896	3	US-09-040-444-6	Sequence 6, Appli
14	686	24.1	1885	3	US-08-501-572-5	Sequence 5, Appli
15	686	24.1	1885	3	US-09-040-444-5	Sequence 5, Appli
16	680.5	23.9	1882	3	US-08-501-572-4	Sequence 4, Appli
17	680.5	23.9	1882	3	US-09-040-444-4	Sequence 4, Appli
18	671	23.6	3213	3	US-09-949-016-1156	Sequence 1156, Ap
19	671	23.6	3213	3	US-09-949-016-4165	Sequence 4165, Ap
20	664.5	23.4	2501	3	US-09-614-891-3	Sequence 3, Appli
21	663.5	23.3	1950	3	US-09-614-891-2	Sequence 2, Appli
22	661	23.2	54550	3	US-10-327-189-42	Sequence 42, Appl
23	654	23.0	1644	3	US-09-949-016-1172	Sequence 1172, Ap
24	653.5	23.0	1954	4	US-10-094-749-1410	Sequence 1410, Ap
25	651	22.9	2907	3	US-09-949-016-5107	Sequence 5107, Ap
c 26	647	22.7	700	3	US-09-735-271-253	Sequence 253, App
27	647	22.7	2121	3	US-09-614-891-4	Sequence 4, Appli
28	647	22.7	25871	3	US-09-798-743-5	Sequence 5, Appli
29	647	22.7	29871	3	US-09-949-016-12180	Sequence 12180, A
30	647	22.7	29876	3	US-09-949-016-13800	Sequence 13800, A
31	635	22.3	614	3	US-10-327-189-8	Sequence 8, Appli
c 32	635	22.3	700	3	US-09-735-271-769	Sequence 769, App
33	635	22.3	26850	3	US-10-327-189-41	Sequence 41, Appl
34	630	22.1	2102	2	US-08-647-397-1	Sequence 1, Appli
35	614.5	21.6	1865	3	US-09-620-312D-271	Sequence 271, App
36	606.5	21.3	1638	3	US-09-572-147-1	Sequence 1, Appli
37	602.5	21.2	1683	5	US-10-114-270-209	Sequence 209, App
38	586	20.6	2123	3	US-09-330-245A-1	Sequence 1, Appli
39	583.5	20.5	2171	4	US-09-424-347B-1	Sequence 1, Appli
40	583.5	20.5	2171	4	US-09-424-347B-3	Sequence 3, Appli
41	575	20.2	2121	3	US-09-614-891-1	Sequence 1, Appli
42	564	19.8	1650	4	US-10-154-419-6	Sequence 6, Appli
43	564	19.8	2206	4	US-10-154-419-4	Sequence 4, Appli
44	564	19.8	2210	3	US-09-786-261-1	Sequence 1, Appli
45	533.5	18.8	2516	4	US-10-094-749-540	Sequence 540, App

ALIGNMENTS

RESULT 1

US-09-521-195B-2

; Sequence 2, Application US/09521195B

; Patent No. 6759514

; GENERAL INFORMATION:

; APPLICANT: Nezu, Jun-Ichi

; APPLICANT: Oku, Asuka

; TITLE OF INVENTION: TRANSPORTER GENES

; FILE REFERENCE: 06501-057001

; CURRENT APPLICATION NUMBER: US/09/521,195B

; CURRENT FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: JP 10/156660

; PRIOR FILING DATE: 1998-05-20

; PRIOR APPLICATION NUMBER: JP 9/260972

; PRIOR FILING DATE: 1997-09-08

; PRIOR APPLICATION NUMBER: PCT/JP98/04009

; PRIOR FILING DATE: 1998-09-07

; NUMBER OF SEQ ID NOS: 33

; SEQ ID NO 2

; LENGTH: 2135

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (147)..(1799)

US-09-521-195B-2

Alignment Scores:

Pred. No.:	0	Length:	2135
Score:	2845.00	Matches:	551
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 10, 2006, 12:03:03 ; Search time 1607 Seconds
(without alignments)
6319.683 Million cell updates/sec

Title: US-10-762-154-1
Perfect score: 2845
Sequence: 1 MRDYDEVIAFLGEWGPQRL.....KKTRDSMETEENPKVLITAF 551

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2833	99.6	2214	9	US-10-327-188-1	Sequence 1, Appli
3	2833	99.6	2214	10	US-10-887-553A-511	Sequence 511, App
4	2783	97.8	2136	9	US-10-327-188-37	Sequence 37, Appl
5	2470	86.8	2083	9	US-10-762-154-23	Sequence 23, Appl
6	2470	86.8	2083	10	US-10-764-420-2373	Sequence 2373, Ap
7	2218	78.0	1831	3	US-09-798-743A-2	Sequence 2, Appli
8	2218	78.0	1831	9	US-10-762-154-4	Sequence 4, Appli
9	2218	78.0	1831	9	US-10-940-500-2	Sequence 2, Appli
10	2218	78.0	1831	10	US-10-955-054A-151	Sequence 151, App
11	2218	78.0	3252	9	US-10-327-188-3	Sequence 3, Appli
12	2218	78.0	3252	10	US-10-887-553A-512	Sequence 512, App
13	2218	78.0	3252	10	US-10-955-054A-7	Sequence 7, Appli
14	2218	78.0	3254	9	US-10-357-930-22299	Sequence 22299, A
15	2218	78.0	3254	9	US-10-357-930-28150	Sequence 28150, A
c 16	2218	78.0	3261	10	US-10-450-763-3020	Sequence 3020, Ap
17	2164	76.1	1888	3	US-09-798-743A-4	Sequence 4, Appli
18	2164	76.1	1888	9	US-10-762-154-28	Sequence 28, Appl
19	2164	76.1	1888	9	US-10-940-500-4	Sequence 4, Appli
20	2164	76.1	2621	10	US-10-764-420-2211	Sequence 2211, Ap
21	2152	75.6	3058	16	US-11-136-527-2498	Sequence 2498, Ap
22	2034.5	71.5	2297	10	US-10-764-420-2012	Sequence 2012, Ap
23	857	30.1	2533	13	US-11-097-143-13628	Sequence 13628, A
24	857	30.1	4533	13	US-11-097-143-13627	Sequence 13627, A
25	819	28.8	2087	13	US-11-097-143-31853	Sequence 31853, A
26	819	28.8	4087	13	US-11-097-143-31852	Sequence 31852, A
27	779.5	27.4	2069	8	US-10-038-854-27	Sequence 27, Appl
28	779.5	27.4	2069	12	US-10-455-772-779	Sequence 779, App
29	773.5	27.2	2030	13	US-11-097-143-9281	Sequence 9281, Ap
30	771.5	27.1	2048	10	US-10-479-013A-1	Sequence 1, Appli
31	753.5	26.5	1666	8	US-10-038-854-29	Sequence 29, Appl
32	753.5	26.5	1666	12	US-10-455-772-781	Sequence 781, App
33	732	25.7	1599	12	US-10-455-772-777	Sequence 777, App
34	706.5	24.8	1725	10	US-10-936-626-27	Sequence 27, Appl
35	706.5	24.8	1725	10	US-10-938-061-27	Sequence 27, Appl
36	705.5	24.8	2257	7	US-10-295-027-299	Sequence 299, App
37	705.5	24.8	2257	10	US-10-936-626-26	Sequence 26, Appl
38	705.5	24.8	2257	10	US-10-938-061-26	Sequence 26, Appl
39	705.5	24.8	2512	8	US-10-712-124-117	Sequence 117, App
40	699.5	24.6	2152	8	US-10-152-319A-1921	Sequence 1921, Ap
41	699.5	24.6	2152	16	US-11-036-196-1921	Sequence 1921, Ap
42	695	24.4	2606	13	US-11-097-143-1409	Sequence 1409, Ap
43	694.5	24.4	1870	9	US-10-643-795A-1	Sequence 1, Appli
44	694.5	24.4	1870	10	US-10-948-518-1	Sequence 1, Appli
45	691.5	24.3	1662	3	US-09-284-320-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-10-762-154-2

; Sequence 2, Application US/10762154

; Publication No. US20040176574A1

; GENERAL INFORMATION:

; APPLICANT: Nezu, Jun-Ichi

; APPLICANT: Oku, Asuka

; TITLE OF INVENTION: TRANSPORTER GENES

; FILE REFERENCE: 06501-057001

; CURRENT APPLICATION NUMBER: US/10/762,154

; CURRENT FILING DATE: 2004-01-21

; PRIOR APPLICATION NUMBER: US/09/521,195B

; PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: JP 10/156660

; PRIOR FILING DATE: 1998-05-20

; PRIOR APPLICATION NUMBER: JP 9/260972

; PRIOR FILING DATE: 1997-09-08

; PRIOR APPLICATION NUMBER: PCT/JP98/04009

; PRIOR FILING DATE: 1998-09-07

; NUMBER OF SEQ ID NOS: 33

; SEQ ID NO 2

; LENGTH: 2135

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

SCORE Search Results Details for Application 10762154 and Search Result us-10-762-154-1.rnpbm.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 10, 2006, 12:06:23 ; Search time 278 Seconds
(without alignments)
4721.383 Million cell updates/sec

Title: US-10-762-154-1
Perfect score: 2845
Sequence: 1 MRDYDEVIAFLGEWGPFQRL.....KKTRDSMETEENPKVLITAF 551

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 4400442

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2833	99.6	2214	8	US-11-266-748A-57212	Sequence 57212, A
3	2783	97.8	2136	8	US-11-318-813-37	Sequence 37, Appl
4	2218	78.0	3252	8	US-11-318-813-3	Sequence 3, Appli
5	2218	78.0	3252	8	US-11-266-748A-22845	Sequence 22845, A
6	2218	78.0	3252	8	US-11-266-748A-29344	Sequence 29344, A
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c 10	1017	35.7	1745	8	US-11-266-748A-370972	Sequence 370972,
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12	865	30.4	668	8	US-11-266-748A-98410	Sequence 98410, A
c 13	865	30.4	668	8	US-11-266-748A-151221	Sequence 151221,
14	865	30.4	933	8	US-11-266-748A-268564	Sequence 268564,
c 15	865	30.4	933	8	US-11-266-748A-329081	Sequence 329081,
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17	706.5	24.8	1725	9	US-11-226-554-27	Sequence 27, Appl
18	706.5	24.8	1725	9	US-11-248-718-27	Sequence 27, Appl
19	705.5	24.8	2257	9	US-11-226-554-26	Sequence 26, Appl
20	705.5	24.8	2257	9	US-11-248-718-26	Sequence 26, Appl
21	691.5	24.3	1902	8	US-11-266-748A-253697	Sequence 253697,
c 22	691.5	24.3	1902	8	US-11-266-748A-314214	Sequence 314214,
23	680	23.9	584	6	US-10-488-619-2766	Sequence 2766, Ap
24	661	23.2	54550	8	US-11-318-813-42	Sequence 42, Appl
25	648	22.8	2527	8	US-11-266-748A-22325	Sequence 22325, A
26	641.5	22.5	4121	8	US-11-266-748A-26550	Sequence 26550, A
27	635	22.3	614	8	US-11-318-813-8	Sequence 8, Appli
28	635	22.3	26850	8	US-11-318-813-41	Sequence 41, Appl
29	626.5	22.0	3987	8	US-11-266-748A-28134	Sequence 28134, A
30	596.5	21.0	2911	8	US-11-266-748A-27051	Sequence 27051, A
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32	528	18.6	713	8	US-11-266-748A-74891	Sequence 74891, A
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c 35	511	18.0	714	8	US-11-266-748A-211571	Sequence 211571,
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ALIGNMENTS

RESULT 1

US-11-318-813-1

; Sequence 1, Application US/11318813

; Publication No. US20060105381A1

; GENERAL INFORMATION:

; APPLICANT: Ellipsis Biotherapeutics Corporation

; APPLICANT: Peltekova, Vanya D

; APPLICANT: Siminovitch, Katherine A

; APPLICANT: St George-Hyslop, Peter H

; APPLICANT: Rubin, Laurence A

; APPLICANT: Peltekova, Vanya D

; APPLICANT: Wintle, Richard F

; TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOCIATED WITH

; TITLE OF INVENTION: INFLAMMATORY BOWEL DISORDERS

; FILE REFERENCE: ELLP-020

; CURRENT APPLICATION NUMBER: US/11/318,813

; CURRENT FILING DATE: 2005-12-27

; PRIOR APPLICATION NUMBER: US/10/327,188

; PRIOR FILING DATE: 2002-12-20

; PRIOR APPLICATION NUMBER: 60/362,700

; PRIOR FILING DATE: 2002-03-08

; PRIOR APPLICATION NUMBER: 60/343,338

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 60/427,529

; PRIOR FILING DATE: 2002-11-19

; PRIOR APPLICATION NUMBER: 60/362,717

; PRIOR FILING DATE: 2002-03-08

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 2214

; TYPE: DNA

SCORE Search Results Details for Application 10762154 and Search Result us-10-762-154-1.rst.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 10, 2006, 11:53:54 ; Search time 7405 Seconds
(without alignments)
6241.368 Million cell updates/sec

Title: US-10-762-154-1
Perfect score: 2845
Sequence: 1 MRDYDEVIAFLGEWGPQRL.....KKTRDSMETEENPKVLITAF 551

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
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- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
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3	2166	76.1	1656	14	AY412017	AY412017 Homo sapi
4	2164	76.1	3077	6	AK167451	AK167451 Mus muscu
5	2159	75.9	3097	6	AK140640	AK140640 Mus muscu
6	2103	73.9	1656	14	AY412019	AY412019 Mus muscu
7	2034.5	71.5	2243	6	AK161508	AK161508 Mus muscu
8	2034.5	71.5	2276	6	AK133431	AK133431 Mus muscu
9	1888.5	66.4	1627	14	AY412018	AY412018 Pan trogl
10	1827	64.2	2506	6	AK080177	AK080177 Mus muscu
11	1388	48.8	832	14	AY412023	AY412023 Homo sapi
12	1346	47.3	832	14	AY412024	AY412024 Pan trogl
13	1283.5	45.1	896	4	BX390610	BX390610 BX390610
14	1270	44.6	933	4	BX709758	BX709758 BX709758
15	1256	44.1	990	1	AL557809	AL557809 AL557809
16	1210	42.5	800	2	BI683731	BI683731 603306292
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18	1160	40.8	954	3	BU200579	BU200579 603949050
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22	1076	37.8	860	5	CF217022	CF217022 AGENCOURT
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26	1062	37.3	796	9	CX489521	CX489521 JGI_XZG32
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36	986	34.7	747	3	BU270255	BU270255 603509303
37	966.5	34.0	799	2	BI647860	BI647860 603276129
38	933	32.8	806	2	BI461374	BI461374 603206838
39	925.5	32.5	879	2	BG870249	BG870249 602791116
40	919	32.3	611	2	BG723644	BG723644 602697810
41	902.5	31.7	1351	9	DN730956	DN730956 CNB55-H03
42	898	31.6	703	4	CB156067	CB156067 K-EST0214
43	893.5	31.4	791	4	CB990521	CB990521 AGENCOURT
44	889	31.2	571	9	DB162581	DB162581 DB162581
45	885	31.1	890	8	CN319141	CN319141 AGENCOURT

ALIGNMENTS

RESULT 1

CR605004

LOCUS CR605004 2149 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CS0DJ003YB03 of T cells (Jurkat cell line)
Cot 10-normalized of Homo sapiens (human).

ACCESSION CR605004

VERSION CR605004.1 GI:50485811

KEYWORDS HTC; CNSLT_cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 2149)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Paraday Avenue

REFERENCE 2 (bases 1 to 2149)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

SCORE Search Results Details for Application 10762154 and Search Result us-10-762-154-2.rge.

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 11:10:17 ; Search time 12183 Seconds
(without alignments)
11206.414 Million cell updates/sec

Title: US-10-762-154-2
Perfect score: 2135
Sequence: 1 ccccggttcgcgcccccaat.....aatactatccaaataaaaaat 2135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: gb_pat:*
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 - 8: gb_sy:*
 - 9: gb_un:*
 - 10: gb_vi:*
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 - 12: gb_htg:*
 - 13: gb_in:*
 - 14: gb_om:*
 - 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
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4	2130.2	99.8	2166	2	CS240059	CS240059 Sequence
5	2130.2	99.8	2166	5	HSPIMTP	Y09881 Homo sapien
6	2130.2	99.8	2214	2	AR533635	AR533635 Sequence
7	2130.2	99.8	2214	2	AX799152	AX799152 Sequence
8	2128.6	99.7	2214	5	BC028313	BC028313 Homo sapi
9	2119.2	99.3	2136	2	CQ721604	CQ721604 Sequence
10	2103.4	98.5	2136	2	AR533668	AR533668 Sequence
11	2103.4	98.5	2136	2	AX799188	AX799188 Sequence

12	1310.6	61.4	2083	2	AR563491	AR563491 Sequence
13	1310.6	61.4	2083	6	AB016257	AB016257 Mus muscu
14	1310.6	61.4	2277	6	BC010590	BC010590 Mus muscu
15	1293	60.6	2258	6	AF169831	AF169831 Rattus no
16	1066.4	49.9	1831	2	CS239323	CS239323 Sequence
17	1066.4	49.9	1831	2	AR563473	AR563473 Sequence
18	1066.4	49.9	1831	2	AR581446	AR581446 Sequence
19	1066.4	49.9	1831	5	AB015050	AB015050 Homo sapi
20	1065.8	49.9	3252	2	CS059038	CS059038 Sequence
21	1065.8	49.9	3252	5	AF057164	AF057164 Homo sapi
22	1065.8	49.9	3254	2	CQ490432	CQ490432 Sequence
23	1065.8	49.9	3254	2	CQ496283	CQ496283 Sequence
24	1064.2	49.8	3252	2	CS239179	CS239179 Sequence
25	1064.2	49.8	3252	2	AR533636	AR533636 Sequence
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31	994	46.6	1888	2	AR563495	AR563495 Sequence
32	994	46.6	1888	2	AR581447	AR581447 Sequence
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34	994	46.6	3111	6	BC031118	BC031118 Mus muscu
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36	983.6	46.1	3007	6	RNAJ1933	AJ001933 Rattus no
37	982.8	46.0	3037	6	AF110416	AF110416 Rattus no
38	978.8	45.8	3038	6	AB017260	AB017260 Rattus no
39	905.6	42.4	2297	6	AB018436	AB018436 Mus muscu
c 40	902.4	42.3	943	7	BV178748	BV178748 sqnm10235
41	808.6	37.9	2243	11	BC056014	BC056014 Xenopus l
42	764.4	35.8	3469	11	CR855437	CR855437 Xenopus t
43	762.8	35.7	2378	11	BC063904	BC063904 Xenopus t
44	658.2	30.8	922	11	BX932928	BX932928 Gallus ga
45	657	30.8	5504	11	BC082839	BC082839 Xenopus l

ALIGNMENTS

RESULT 1

CS059053

LOCUS CS059053 2135 bp DNA linear PAT 13-APR-2005

DEFINITION Sequence 1 from Patent WO2005026737.

ACCESSION CS059053

VERSION CS059053.1 GI:62551899

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS Golz,S., Brueggemeier,U. and Geerts,A.

TITLE Diagnostics and therapeutics for diseases associated with
organisation transporter slc22a4 (slc22a4)JOURNAL Patent: WO 2005026737-A 1 24-MAR-2005;
Bayer HealthCare AG (DE)

FEATURES

Location/Qualifiers

source

1..2135

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/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 2135; DB 2; Length 2135;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	121	CAAGTTTCGGAGCGGCAGTGGGAAGCATGCGGGACTACGACGAGGTGATCGCCTTCCTGG	180
Db	121	CAAGTTTCGGAGCGGCAGTGGGAAGCATGCGGGACTACGACGAGGTGATCGCCTTCCTGG	180
Qy	181	GCGAGTGGGGCCCTTCCAGCGCCTCATCTTCTTCTGCTCAGGCCAGCATCATCCCCA	240

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 11:09:17 ; Search time 1348 Seconds
(without alignments)
11042.842 Million cell updates/sec

Title: US-10-762-154-2
Perfect score: 2135
Sequence: 1 ccccggtctcgcgccccaat.....aatactatccaaataaaaat 2135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 4: geneseqn2001as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	2130.2	99.8	2135	8	ABZ24258	Abz24258 Human SLC
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7	2130.2	99.8	2214	14	ADZ49182	Adz49182 Insulin s
8	2103.4	98.5	2136	9	ACF05052	Acf05052 Human cat
9	1736	81.3	1736	8	ABZ24259	Abz24259 Human SLC
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11	1310.6	61.4	2083	14	ADZ62649	Adz62649 Murine Sl

12	1066.4	49.9	1831	2	AAX26880	Aax26880 DNA encod
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14	1066.4	49.9	1831	8	ABZ24261	Abz24261 Human SLC
15	1066.4	49.9	1831	8	ACD13415	Acd13415 Human DNA
16	1066.4	49.9	1831	15	AEE60942	Aee60942 Human pat
17	1066.4	49.9	3051	10	ADE07453	Ade07453 Novel cod
c 18	1066.4	49.9	3261	5	AAS67216	Aas67216 DNA encod
c 19	1066.4	49.9	3261	10	ADE09665	Ade09665 Novel DNA
c 20	1066.4	49.9	3261	10	ADE09605	Ade09605 Novel DNA
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23	1065.8	49.9	3252	14	ADY79866	Ady79866 Nucleotid
24	1065.8	49.9	3254	5	ABV22306	Abv22306 Human pro
25	1065.8	49.9	3254	5	ABV28137	Abv28137 Human pro
26	1064.2	49.8	3252	14	ADZ49183	Adz49183 Insulin s
27	1064.2	49.8	3252	15	AEE60798	Aee60798 Human pat
28	1062.6	49.8	2811	8	ABZ24260	Abz24260 Human SLC
29	1057.2	49.5	1674	14	ADV43783	Adv43783 Human psy
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31	994	46.6	1888	3	AAA09890	Aaa09890 Mouse OCT
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34	982.8	46.0	3037	10	ADB52930	Adb52930 Primary r
35	978.8	45.8	3038	12	ADP71869	Adp71869 Renal tox
36	905.6	42.4	2297	3	AAA88053	Aaa88053 Mouse OCT
37	905.6	42.4	2297	14	ADZ62288	Adz62288 Murine Sl
38	523.4	24.5	54550	9	ACF05021	Acf05021 Human cat
c 39	505	23.7	700	4	AAH92757	Aah92757 Human inf
40	462	21.6	2928	12	ADL17760	Adl17760 Organic c
c 41	363.8	17.0	700	4	AAH92241	Aah92241 Human inf
42	363.8	17.0	25871	3	AAA09888	Aaa09888 Human gen
43	360.2	16.9	26850	9	ACF05020	Acf05020 Human cat
c 44	314	14.7	700	4	AAH92293	Aah92293 Human inf
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ALIGNMENTS

RESULT 1

AAX26879

ID AAX26879 standard; DNA; 2135 BP.

XX

AC AAX26879;

XX

DT 23-JUN-1999 (first entry)

XX

DE DNA encoding a protein with cation transporting activity.

XX

KW Organic cation transporter; OCT1; OCT2; drug development; fatty liver;

KW heart disease; cancer; anti-tumour drug; anticancer drug; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 147..1802

FT /*tag= a

XX

PN WO9913072-A1.

XX

PD 18-MAR-1999.

XX

PF 07-SEP-1998; 98WO-JP004009.

XX

PR 08-SEP-1997; 97JP-00260972.

PR 20-MAY-1998; 98JP-00156660.

XX

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX

PI Nezu J, Oku A;

XX

DR WPI; 1999-215062/18.

DR P-PSDB; AAY01649.

XX

PT Genes homologous with organic cation transporters OCT1 and OCT2, useful

PT in design of new drugs for treatment of diseases due to abnormality of

PT the transporter functions.

XX

PS Claim 2; Page 45-51; 97pp; Japanese.

XX

CC The present sequence encodes a protein with cation transporting activity.

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 11:14:03 ; Search time 559 Seconds
(without alignments)
7146.364 Million cell updates/sec

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Perfect score: 2135
Sequence: 1 ccccggtctcgcgccccaat.....aatactatccaataaaaat 2135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

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Listing first 45 summaries

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	2	2130.2	99.8	2214	3	US-10-327-189-1	Sequence 1, Appli
	3	2103.4	98.5	2136	3	US-10-327-189-37	Sequence 37, Appl
	4	1310.6	61.4	2083	3	US-09-521-195B-23	Sequence 23, Appl
	5	1066.4	49.9	1831	3	US-09-521-195B-4	Sequence 4, Appli
	6	1066.4	49.9	1831	3	US-09-798-743-2	Sequence 2, Appli
	7	1065.8	49.9	3252	3	US-09-949-016-438	Sequence 438, App
	8	1064.2	49.8	3252	3	US-10-327-189-3	Sequence 3, Appli
	9	1023	47.9	3223	3	US-09-949-016-2058	Sequence 2058, Ap
	10	994	46.6	1888	3	US-09-521-195B-28	Sequence 28, Appl
	11	994	46.6	1888	3	US-09-798-743-4	Sequence 4, Appli
	12	526.4	24.7	54550	3	US-10-327-189-42	Sequence 42, Appl
c	13	505	23.7	700	3	US-09-735-271-769	Sequence 769, App
	14	364.8	17.1	29871	3	US-09-949-016-12180	Sequence 12180, A
	15	364.8	17.1	29876	3	US-09-949-016-13800	Sequence 13800, A
c	16	363.8	17.0	700	3	US-09-735-271-253	Sequence 253, App

17	363.8	17.0	25871	3	US-09-798-743-5	Sequence 5, Appli
18	360.2	16.9	614	3	US-10-327-189-8	Sequence 8, Appli
19	360.2	16.9	26850	3	US-10-327-189-41	Sequence 41, Appl
c 20	314	14.7	700	3	US-09-735-271-305	Sequence 305, App
c 21	297	13.9	700	3	US-09-735-271-306	Sequence 306, App
c 22	234	11.0	700	3	US-09-735-271-768	Sequence 768, App
c 23	217.6	10.2	700	3	US-09-735-271-689	Sequence 689, App
24	195.2	9.1	1896	3	US-08-501-572-6	Sequence 6, Appli
25	195.2	9.1	1896	3	US-09-040-444-6	Sequence 6, Appli
c 26	184	8.6	700	3	US-09-735-271-687	Sequence 687, App
27	177	8.3	601	3	US-09-949-016-26460	Sequence 26460, A
28	177	8.3	601	3	US-09-949-016-69832	Sequence 69832, A
c 29	176	8.2	700	3	US-09-735-271-714	Sequence 714, App
30	175	8.2	1882	3	US-08-501-572-4	Sequence 4, Appli
31	175	8.2	1882	3	US-09-040-444-4	Sequence 4, Appli
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c 35	158.4	7.4	700	3	US-09-735-271-731	Sequence 731, App
36	150.8	7.1	1865	3	US-09-620-312D-271	Sequence 271, App
c 37	150	7.0	700	3	US-09-735-271-222	Sequence 222, App
38	146.6	6.9	601	3	US-09-949-016-26459	Sequence 26459, A
39	146.6	6.9	601	3	US-09-949-016-69831	Sequence 69831, A
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41	143.2	6.7	2501	3	US-09-614-891-3	Sequence 3, Appli
c 42	140.2	6.6	700	3	US-09-735-271-1285	Sequence 1285, Ap
43	136.8	6.4	1683	5	US-10-114-270-209	Sequence 209, App
44	135.6	6.4	136	3	US-10-327-189-36	Sequence 36, Appl
45	134.2	6.3	2121	3	US-09-614-891-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-521-195B-2

; Sequence 2, Application US/09521195B

; Patent No. 6759514

; GENERAL INFORMATION:

; APPLICANT: Nezu, Jun-Ichi

; APPLICANT: Oku, Asuka

; TITLE OF INVENTION: TRANSPORTER GENES

; FILE REFERENCE: 06501-057001

; CURRENT APPLICATION NUMBER: US/09/521,195B

; CURRENT FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: JP 10/156660

; PRIOR FILING DATE: 1998-05-20

; PRIOR APPLICATION NUMBER: JP 9/260972

; PRIOR FILING DATE: 1997-09-08

; PRIOR APPLICATION NUMBER: PCT/JP98/04009

; PRIOR FILING DATE: 1998-09-07

; NUMBER OF SEQ ID NOS: 33

; SEQ ID NO 2

; LENGTH: 2135

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (147)..(1799)

US-09-521-195B-2

Query Match 100.0%; Score 2135; DB 3; Length 2135;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     61 CTTGGGGAGCGCCCCAGCTACAAGACACTGTCTGAGAACGCTGTCATACCCGTTAGTTG 120
      |||
Db     61 CTTGGGGAGCGCCCCAGCTACAAGACACTGTCTGAGAACGCTGTCATACCCGTTAGTTG 120

Qy    121 CAAGTTTCGGAGCGGCAGTGGGAAGCATGCGGGACTACGACGAGGTGATCGCTTCCTGG 180
      |||
Db    121 CAAGTTTCGGAGCGGCAGTGGGAAGCATGCGGGACTACGACGAGGTGATCGCTTCCTGG 180

Qy    181 GCGAGTGGGGGCCCTTCAGCGCCTCATCTTCTTCTGCTCAGCGCCAGCATCATCCCCA 240
      |||
Db    181 GCGAGTGGGGGCCCTTCAGCGCCTCATCTTCTTCTGCTCAGCGCCAGCATCATCCCCA 240

```

SCORE Search Results Details for Application 10762154 and Search Result us-10-762-154-2.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 11:32:58 ; Search time 2686 Seconds
(without alignments)
9766.977 Million cell updates/sec

Title: US-10-762-154-2
Perfect score: 2135
Sequence: 1 ccccggttcgcgcccgaat.....aatactatccaaataaaaat 2135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : **Published Applications_NA_Main:***
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2135	100.0	2135	9	US-10-762-154-2	Sequence 2, Appli
2	2130.2	99.8	2214	9	US-10-327-188-1	Sequence 1, Appli
3	2130.2	99.8	2214	10	US-10-887-553A-511	Sequence 511, App
4	2103.4	98.5	2136	9	US-10-327-188-37	Sequence 37, Appl
5	1310.6	61.4	2083	9	US-10-762-154-23	Sequence 23, Appl
6	1310.6	61.4	2083	10	US-10-764-420-2373	Sequence 2373, Ap
7	1066.4	49.9	1831	3	US-09-798-743A-2	Sequence 2, Appli
8	1066.4	49.9	1831	9	US-10-762-154-4	Sequence 4, Appli
9	1066.4	49.9	1831	9	US-10-940-500-2	Sequence 2, Appli
10	1066.4	49.9	1831	10	US-10-955-054A-151	Sequence 151, App

c	11	1066.4	49.9	3261	10	US-10-450-763-3020	Sequence 3020, Ap
	12	1065.8	49.9	3254	9	US-10-357-930-22299	Sequence 22299, A
	13	1065.8	49.9	3254	9	US-10-357-930-28150	Sequence 28150, A
	14	1064.2	49.8	3252	9	US-10-327-188-3	Sequence 3, Appli
	15	1064.2	49.8	3252	10	US-10-887-553A-512	Sequence 512, App
	16	1064.2	49.8	3252	10	US-10-955-054A-7	Sequence 7, Appli
	17	994	46.6	1888	3	US-09-798-743A-4	Sequence 4, Appli
	18	994	46.6	1888	9	US-10-762-154-28	Sequence 28, Appl
	19	994	46.6	1888	9	US-10-940-500-4	Sequence 4, Appli
	20	992.4	46.5	2621	10	US-10-764-420-2211	Sequence 2211, Ap
	21	982	46.0	3058	16	US-11-136-527-2498	Sequence 2498, Ap
	22	905.6	42.4	2297	10	US-10-764-420-2012	Sequence 2012, Ap
	23	526.4	24.7	54550	9	US-10-327-188-42	Sequence 42, Appl
	24	363.8	17.0	25871	3	US-09-798-743A-5	Sequence 5, Appli
	25	363.8	17.0	25871	9	US-10-940-500-5	Sequence 5, Appli
	26	360.2	16.9	614	9	US-10-327-188-8	Sequence 8, Appli
	27	360.2	16.9	26850	9	US-10-327-188-41	Sequence 41, Appl
c	28	274.2	12.8	551	9	US-10-363-345A-32559	Sequence 32559, A
	29	274.2	12.8	551	9	US-10-363-345A-32560	Sequence 32560, A
c	30	274.2	12.8	551	10	US-10-363-483A-32559	Sequence 32559, A
	31	274.2	12.8	551	10	US-10-363-483A-32560	Sequence 32560, A
	32	242.2	11.3	551	9	US-10-363-345A-32557	Sequence 32557, A
c	33	242.2	11.3	551	9	US-10-363-345A-32558	Sequence 32558, A
	34	242.2	11.3	551	10	US-10-363-483A-32557	Sequence 32557, A
c	35	242.2	11.3	551	10	US-10-363-483A-32558	Sequence 32558, A
	36	218	10.2	554	7	US-10-029-386-4720	Sequence 4720, Ap
	37	213.4	10.0	215	7	US-10-029-386-18476	Sequence 18476, A
	38	198	9.3	2186	16	US-11-136-527-2958	Sequence 2958, Ap
	39	195.6	9.2	2152	8	US-10-152-319A-1921	Sequence 1921, Ap
	40	195.6	9.2	2152	16	US-11-036-196-1921	Sequence 1921, Ap
	41	193.6	9.1	1725	10	US-10-936-626-27	Sequence 27, Appl
	42	193.6	9.1	1725	10	US-10-938-061-27	Sequence 27, Appl
	43	193.6	9.1	2257	7	US-10-295-027-299	Sequence 299, App
	44	193.6	9.1	2257	10	US-10-936-626-26	Sequence 26, Appl
	45	193.6	9.1	2257	10	US-10-938-061-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-10-762-154-2

; Sequence 2, Application US/10762154

; Publication No. US20040176574A1

; GENERAL INFORMATION:

; APPLICANT: Nezu, Jun-Ichi

; APPLICANT: Oku, Asuka

; TITLE OF INVENTION: TRANSPORTER GENES

; FILE REFERENCE: 06501-057001

; CURRENT APPLICATION NUMBER: US/10/762,154

; CURRENT FILING DATE: 2004-01-21

; PRIOR APPLICATION NUMBER: US/09/521,195B

; PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: JP 10/156660

; PRIOR FILING DATE: 1998-05-20

; PRIOR APPLICATION NUMBER: JP 9/260972

; PRIOR FILING DATE: 1997-09-08

; PRIOR APPLICATION NUMBER: PCT/JP98/04009

; PRIOR FILING DATE: 1998-09-07

; NUMBER OF SEQ ID NOS: 33

; SEQ ID NO 2

; LENGTH: 2135

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (147)..(1799)

US-10-762-154-2

Query Match 100.0%; Score 2135; DB 9; Length 2135;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CCCCCGCTTCGCGCCCAATTTCTAACAGCCTGCCTGTCCCCGGGAACGTTCTAACATC 60

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Db 61 CTTGGGGAGCGCCCCAGCTACAAGACACTGTCCTGAGAACGCTGTCATACCCGTAGTTG 120

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 11:39:12 ; Search time 387 Seconds
(without alignments)
8761.089 Million cell updates/sec

Title: US-10-762-154-2
Perfect score: 2135
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2200221 seqs, 794037843 residues

Total number of hits satisfying chosen parameters: 4400442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
- 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
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		Match	Length			
1	2130.2	99.8	2214	8	US-11-318-813-1	Sequence 1, Appli
2	2130.2	99.8	2214	8	US-11-266-748A-57212	Sequence 57212, A
3	2103.4	98.5	2136	8	US-11-318-813-37	Sequence 37, Appl
4	1065.8	49.9	3252	8	US-11-266-748A-22845	Sequence 22845, A
5	1064.2	49.8	3252	8	US-11-318-813-3	Sequence 3, Appli
6	1064.2	49.8	3252	8	US-11-266-748A-29344	Sequence 29344, A
7	1064.2	49.8	3252	8	US-11-266-748A-57187	Sequence 57187, A
8	936.8	43.9	1000	8	US-11-266-748A-396119	Sequence 396119,
c 9	936.8	43.9	1000	8	US-11-266-748A-467165	Sequence 467165,
10	835.8	39.1	933	8	US-11-266-748A-268564	Sequence 268564,
c 11	835.8	39.1	933	8	US-11-266-748A-329081	Sequence 329081,
12	656.4	30.7	713	8	US-11-266-748A-74891	Sequence 74891, A
c 13	656.4	30.7	713	8	US-11-266-748A-127702	Sequence 127702,
c 14	648.8	30.4	714	8	US-11-266-748A-211571	Sequence 211571,
15	648.8	30.4	714	8	US-11-266-748A-235211	Sequence 235211,
16	610.8	28.6	668	8	US-11-266-748A-98410	Sequence 98410, A

c	17	610.8	28.6	668	8	US-11-266-748A-151221	Sequence 151221,
c	18	528	24.7	1745	8	US-11-266-748A-370972	Sequence 370972,
	19	528	24.7	1745	8	US-11-266-748A-454351	Sequence 454351,
	20	526.4	24.7	54550	8	US-11-318-813-42	Sequence 42, Appl
	21	360.2	16.9	614	8	US-11-318-813-8	Sequence 8, Appli
	22	360.2	16.9	26850	8	US-11-318-813-41	Sequence 41, Appl
c	23	336	15.7	371	8	US-11-266-748A-2307	Sequence 2307, Ap
	24	336	15.7	371	8	US-11-266-748A-62946	Sequence 62946, A
c	25	336	15.7	371	8	US-11-266-748A-65778	Sequence 65778, A
	26	285	13.3	399	8	US-11-266-748A-179338	Sequence 179338,
	27	267.2	12.5	584	6	US-10-488-619-2766	Sequence 2766, Ap
	28	193.6	9.1	1725	9	US-11-226-554-27	Sequence 27, Appl
	29	193.6	9.1	1725	9	US-11-248-718-27	Sequence 27, Appl
	30	193.6	9.1	2257	9	US-11-226-554-26	Sequence 26, Appl
	31	193.6	9.1	2257	9	US-11-248-718-26	Sequence 26, Appl
	32	187.8	8.8	1983	8	US-11-266-748A-56737	Sequence 56737, A
	33	184.4	8.6	1902	8	US-11-266-748A-253697	Sequence 253697,
c	34	184.4	8.6	1902	8	US-11-266-748A-314214	Sequence 314214,
c	35	177	8.3	1065	8	US-11-266-748A-5959	Sequence 5959, Ap
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c	37	177	8.3	1065	8	US-11-266-748A-66327	Sequence 66327, A
	38	135.6	6.4	136	8	US-11-318-813-36	Sequence 36, Appl
	39	133.4	6.2	2527	8	US-11-266-748A-22325	Sequence 22325, A
	40	133.2	6.2	4121	8	US-11-266-748A-26550	Sequence 26550, A
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	42	128.8	6.0	1000	8	US-11-266-748A-403278	Sequence 403278,
c	43	128.8	6.0	1000	8	US-11-266-748A-474324	Sequence 474324,
c	44	128.8	6.0	1000	8	US-11-266-748A-481659	Sequence 481659,
	45	122.8	5.8	3987	8	US-11-266-748A-28134	Sequence 28134, A

ALIGNMENTS

RESULT 1

US-11-318-813-1

; Sequence 1, Application US/11318813

; Publication No. US20060105381A1

; GENERAL INFORMATION:

; APPLICANT: Ellipsis Biotherapeutics Corporation

; APPLICANT: Peltekova, Vanya D

; APPLICANT: Siminovitch, Katherine A

; APPLICANT: St George-Hyslop, Peter H

; APPLICANT: Rubin, Laurence A

; APPLICANT: Peltekova, Vanya D

; APPLICANT: Wintle, Richard F

; TITLE OF INVENTION: POLYMORPHISMS OF THE OCTN1 AND OCTN2 CATION TRANSPORTERS ASSOCIATED WITH

; TITLE OF INVENTION: INFLAMMATORY BOWEL DISORDERS

; FILE REFERENCE: ELLP-020

; CURRENT APPLICATION NUMBER: US/11/318,813

; CURRENT FILING DATE: 2005-12-27

; PRIOR APPLICATION NUMBER: US/10/327,188

; PRIOR FILING DATE: 2002-12-20

; PRIOR APPLICATION NUMBER: 60/362,700

; PRIOR FILING DATE: 2002-03-08

; PRIOR APPLICATION NUMBER: 60/343,338

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 60/427,529

; PRIOR FILING DATE: 2002-11-19

; PRIOR APPLICATION NUMBER: 60/362,717

; PRIOR FILING DATE: 2002-03-08

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 2214

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (166)..(1821)

; OTHER INFORMATION:

US-11-318-813-1

Query Match 99.8%; Score 2130.2; DB 8; Length 2214;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2132; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	CCCCGGCTTCGCGCCCAATTCTTAACAGCCTGCCTGTCCCCGGGAACGTTCTAACATC	60
Db	20	CCCCGGCTTCGCGCCCAATTCTTAACAGCCTGCCTGTCCCCGGGAACGTTCTAACATC	79

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2006, 11:11:24 ; Search time 15148 Seconds
(without alignments)
7881.421 Million cell updates/sec

Title: US-10-762-154-2
Perfect score: 2135
Sequence: 1 ccccggttcgcgcgcccaat.....aatactatccaaataaaaat 2135

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : **EST:***

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2116.2	99.1	2149	6 CR605004	CR605004 full-leng
2	1107	51.9	2169	6 AK143595	AK143595 Mus muscu
3	1016	47.6	1656	14 AY412017	AY412017 Homo sapi
4	994	46.6	3077	6 AK167451	AK167451 Mus muscu
5	992.4	46.5	3097	6 AK140640	AK140640 Mus muscu
c 6	942.2	44.1	1016	1 AL557808	AL557808 AL557808
7	940.6	44.1	1656	14 AY412019	AY412019 Mus muscu
8	905.6	42.4	2243	6 AK161508	AK161508 Mus muscu
9	905.6	42.4	2276	6 AK133431	AK133431 Mus muscu
10	891	41.7	1627	14 AY412018	AY412018 Pan trogl
11	886.2	41.5	990	1 AL557809	AL557809 AL557809
12	827.2	38.7	832	14 AY412023	AY412023 Homo sapi

13	811.8	38.0	832	14	AY412024	AY412024	Pan trogl
14	758.8	35.5	896	4	BX390610	BX390610	BX390610
15	722.8	33.9	2506	6	AK080177	AK080177	Mus muscu
16	695.6	32.6	703	4	CB156067	CB156067	K-EST0214
c 17	654	30.6	668	5	CD616183	CD616183	56080808J
c 18	648.8	30.4	714	3	BU687273	BU687273	UI-CF-EC1
c 19	645.2	30.2	725	3	BM984651	BM984651	UI-CF-EC1
20	641.6	30.1	832	14	AY412025	AY412025	Mus muscu
21	594.2	27.8	637	5	CF132623	CF132623	UI-HF-FQ0
22	575.6	27.0	726	1	AJ816823	AJ816823	AJ816823
23	562.6	26.4	800	2	BI683731	BI683731	603306292
24	556.8	26.1	588	5	CF132525	CF132525	UI-HF-FQ0
25	552.4	25.9	954	3	BU200579	BU200579	603949050
26	542	25.4	573	9	DA076329	DA076329	DA076329
27	535.6	25.1	910	2	BI552541	BI552541	603194456
28	534	25.0	564	9	DB198884	DB198884	DB198884
c 29	528.8	24.8	559	1	AI032763	AI032763	ox13h02.x
c 30	521.2	24.4	613	7	AW264315	AW264315	xq98b08.x
31	520	24.4	583	9	DA670486	DA670486	DA670486
32	518	24.3	562	9	DA475196	DA475196	DA475196
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37	507.4	23.8	572	9	DA372428	DA372428	DA372428
38	506	23.7	569	9	DA633580	DA633580	DA633580
c 39	505.4	23.7	544	7	AW592711	AW592711	hf46e06.x
40	501	23.5	579	9	DA276275	DA276275	DA276275
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43	493	23.1	559	9	DA542922	DA542922	DA542922
44	492.8	23.1	571	9	DA955623	DA955623	DA955623
45	490.6	23.0	611	2	BG723644	BG723644	602697810

ALIGNMENTS

RESULT 1
CR605004
LOCUS CR605004 2149 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DJ003YB03 of T cells (Jurkat cell line)
Cot 10-normalized of Homo sapiens (human).
ACCESSION CR605004
VERSION CR605004.1 GI:50485811
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 2149)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
REFERENCE 2 (bases 1 to 2149)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES Location/Qualifiers
source 1..2149
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ003YB03"
/tissue_type="T cells (Jurkat cell line) Cot
10-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 99.1%; Score 2116.2; DB 6; Length 2149;